



1/8

GGGGGATCATGGAAGCTGATAAAGATGACACACAACAAATTCTTAAGGAGCATTGCCAGATGAA
TTTATAAAAGATGAACAAAATAAGGGACTAATTGATGAAATTACAAAGAAAAATATTCAACTAAA
GAAGGAGATCCAAAAGCTTGAAACGGAGTTACAAGAGGCTACCAAAGAATTCCAGATTAAAGAGG
ATATTCCTGAAACAAAGATGAAATTCTTATCAGTTGAAACTCCTGAGAATGACAGCCAGTTGTCA
AATATCTCCTGTTTCGTTTCAAGTGAGCTCGAAAGTTCCTTATGAGATACAAAAGGACAAGCACT
TATCACCTTTGAAAAAGAAGAAGTTGCTCAAATGTGGTAAGCATGAGTAAACATCATGTACAGA
TAAAAGATGTAAATCTGGAGGTTACGGCCAAGCCAGTTCCATTAAATTCAGGAGTCAGATTCCAG
GTTTATGTAGAAGTTTCTAAAATGAAAATCAATGTTACTGAAATTCCTGACACATTGCGTGAAGA
TCAAATGAGAGACAACTAGAGCTGAGCTTTTCAAAGTCCCGAAATGGGAGGCGGAGANGTGGAC
CGCGTGGGACTATGACAGACAGTCCGGGAGTGCAGTCATCACGTTTGGNGGAGATTGGGAGTGGC
TGACANN (SEQ ID NO:4)

Figure 1

Hou c6/#1



2/8

CGGAGTTACAAGAGGCTACCAAAGAATTCCAGATTAAAGAGGATATTCCTGAAACAAAGATGAAA
TTCTTATCAGTTGAAACTCCTGANAATGACAGCCAGTTGTCAAATATCTCCTGTTTCGTTTCAAGG
TGAGCTCGAAAGTTCCTTATGAGATACAAAAAGGACAATGCACTTATCACCTTTGAAAAAGGAAG
AAGTTGCTCAAAATGTGNGTAANGCATGAGTAAACATCATGTACAGATAATAAGATGTAAATCTG
GAGGTTACGGCCAAAGCCAAGTTCCTTAATATTCAAGGAGTCANGATTCCAGNGTTTATGCTAG
AANGTTTCTAAAAATGANAATCAATGGTTACTGGAAATTCTTGGACACATTGCGNTGAAAGATCA
AGATGACGAAGACAACTAAGAAGCTGAGCTTTTCAAAGTCCCGAAANATGGAAGAGCGGTAGA
GGGTGGNACCGCGTGNGANCTATGACAAGACAAGNCCGGGGAAGNTGCAGTCCATCACGTTTGTN
NGAAGATTGGANGTNGGCTGACCAANGAATTTTGAAAAAGGAGANGAATTACCCCTCTTTANGAG
TAANATCAAAACCCTGCCATAANAAGTTNACTGGTTTCNCCCATTACACAGNAN
TTACANNTTGANCAANANTANNCAGGATAATTTNCAGGGGAANAATCTNAAGNATGGCAAGNTGA
CTTCTGGACAANGGT (SEQ ID NO:5)

Figure 2

Hou c17/#2



c6/#1	1	HEGRGI	MEADKDDTQQILKEHSPDEFIKDEQNKGLIDEITKKNIQLKKEI	OKLETELQEA
Hou/Nmi	1	-----	MEADKDDTQQILKEHSPDEFIKDEQNKGLIDEITKKNIQLKKEI	OKLETELQEA
c6/#1	61	TKEFQIKEDIPETKMKFLSVETPENDS	QLSNISCSFQVSSKVPYEIQKQALITFEKEEV	
Hou/Nmi	55	TKEFQIKEDIPETKMKFLSVETPENDS	QLSNISCSFQVSSKVPYEIQKQALITFEKEEV	
c6/#1	121	AQNVVSMKHHVQIKDVNLEVTAKPVPLNSGVRFQVYVEVSKMKIN	VTETIPDTLREDQMR	
Hou/Nmi	115	AQNVVSMKHHVQIKDVNLEVTAKPVPLNSGVRFQVYVEVSKMKIN	VTETIPDTLREDQMR	
c6/#1	181	DKLELSFSKSRNGRRRCGP	RGTMDSFGVQSSRLVEIGS	-----
Hou/Nmi	175	DKLELSFSKSRNGGGEV.D	VDYDRQS	SAVITFVEIGV DKILAKKEYPLYINQTCHRV
c6/#1	221	-----	-----	-----
Hou/Nmi	234	TVSPYTEIHLKKYQIFSGTSKRTVLLTGMEGIQMDREIVED	LINEHPQRAKNGGGEVDVV	
c6/#1	221	-----	(SEQ ID NO:6)	
Hou/Nmi	294	KCSLGQPFIAYFEE	(SEQ ID NO:7)	

Figure 3



4/8

AGCAGGTGCTGCAACAAAAGGAGCACACGATCAACATGGAGGAGTGCCGGCTGCGGGTGCAGGTC
CAGCCCTTGGAGCTGCCCATGGTCACCACCATCCAGGTGTCCAGCCAGTTGAGTGGCCGGAGGGT
GTTGGTCACTGGATTTCCCTGCCAGCCTCAGGCTGAGTGAGGAGGAGCTGCTGGACAANCTANAGA
TCTTCTTTGGCAAGACTAGGAACGGAGGTGGCNATGTGGACNTTCGGGANCTACTGCCAGGGANT
GTCATGCTGGGGTTTGTAGGGATGGAGTGGCTCANCCTGTGTGCCAAATCGGCCATTTACAGT
GCCACTGGGTGGGCAGCANGTCCCTCTGAGAGTCTCTCCGTATGTGAATGGGGANATCCAGANGG
CTGANATCAGGTCNCAGCCANTTCCCCGCTCGGTACTGGTGCTCAACATTCTTGATATCTTGGAT
GGCCCGGAGCTGCATGACGTCCTGGANATCCACTTCCAGAANCCACCCGCGGGGGCGGAGATGT
AAGACGCCCTGACAGTCGTACCCCAAGGACAACAGGGCCTAACAGTCTTCACCTCCTGAATCAAG
GCTANGGGCCTCCCCCTTCTCATCCTCCCCACCCCCCGCCAAAGGTTCTCAANACTGGGCCTG
GGCTTTNTG (SEQ ID NO:8)

Figure 4

IFP35 c14/#1



5/8

CCAAAGTGGCTGAGCAGGTGCTGCAACAAAAGGAGCACACGATCAACATGGAGGAGTGCCGGCTGCGGGTGC
AGGTCCAGCCCTTGGAGCTGCCCATGGTCACCACCATCCAGGTGTCCAGCCAGTTGAGTGGCCGGAGGGTGT
TGGTCACTGGATTTCTGCCAGCCTCAGGCTGAGTGAGGAGGAGCTGCTGGACAAGCTAGAGATCTTCTTTG
GCAAGACTAGGAACGGAGGTGGCGATGTGGACGTTCTGGGAGCTACTGCCAGGGAGTGTGCTGCTGGGGTTTG
CTAGGGATGGAGTGGCTCAGCGTCTGTGCCAAATCGGCCAAGTTCACAGTGCCACTGGGTGGGCANCAAGTC
CCTCTGAGAGTCTCTCCGTATGTGAATGGGGAGATCCAGAAGGCTGAGATCAGGTTCGCANCCAGTTCCCCNC
TCGGTACTGGGTGCTCAACATTCCTGATATCTTGGATTGGCCCGGAGCTGCATNACGTCCTGGANATCAACT
TCANAAGCCCACCCGCCGGGCGNGAGGTANAAGGCCTGACATCNTTACCCCAAAGGACAGCATGGNCCTA
ACAGTCCTCACCTCCNAATCANGCTNNGGGGCTNCCCTTCTANCNTCCCCAACTG (SEQ ID NO:9)

Figure 5

IFP35 c33/#2



6/8

GGATCCACTGCCCTCTGCTTGCGGGCTCTGCTCTGATCACCTTTGATGACCCCAAAGTGGCTGAG
CAGGTGCTGCAACAAAAGGAGCACACGATCAACATGGAGGAGTGCCGGCTGCGGGTGCAGGTCCA
GCCCTTGGAGCTGCCCATGGTCACCACCATCCAGGTGATGGTGTCCAGCCANTTGAGTGGCCGGA
GGGTGTTGGTCACTGGATTTCTGCCAGCCTCAGGCTGANTGAGGAGGAGCTGCTGGACAAGCTA
TGAGATCTTCTTTGGCAANACTANGAACGGANGTGGCGATGTGGACGTTTCGGGAGCTACTGCCAG
GGAGTGTGATGCTGGGGTTTGCTACGGATGGAGTGGCTCAGCGTCTGTGCCAAATCGGCCAGTTC
ACAAGTGCCACTGGGTGGGCAGCAAGTCCCTCTGAGAGTCTCTCCGTATGTGANTGGNGAGATCA
GAATGCTGANATTAAGTCGCATCCAATTCCTCGCTCNGGTACTGGTGCTCANNATCCTGANATCT
TGGATTGGCCCCNGANTNCATGANATCTGGNAGATTCAATTNCANAAGTCCANCCNNCNGNGNCG
GGAAGTANANGCCCGANANTTCNTNNCNTANGGNCAGCANNGCCTG (SEQ ID NO:10)

Figure 6

IFP35 c51/#3



```
331fn 1 -----MSAPLDAALHAQZQARLKMRLWDLQQLRKLQDSPKDKVPFSPVKIPLVFRGHTQQDP-----
In35_Human 1
CS1 1

331fn 1 -----HGPCKVAEQVLQCKEHTINHEECRLRVQVQPLELPM-----
In35_Human 61 EVPKSLVSNLRHCPCLLAGSALITFDDPKVAEQVLQCKEHTINHEECRLRVQVQPLELPM-----
CS1 1 -----HECRIHCPCLLAGSALITFDDPKVAEQVLQCKEHTINHEECRLRVQVQPLELPM-----

331fn 37 VTTIQ..VSSQLSGRRVLVTGFPASLRLSEELLDKLEIFFGKTRNGGGDGDVRELLPGS-----
In35_Human 121 VTTIQ..VSSQLSGRRVLVTGFPASLRLSEELLDKLEIFFGKTRNGGGDGDVRELLPGS-----
CS1 54 VTTIQVMVSSLSGRRVLVTGFPASLRLSEELLDKLEIFFGKTRNGGGDGDVRELLPGS.....

331fn 95 VMLGFARDGVAQRLLCOICQVHSAFCWASSPSZSHSVCEMCDPEQ-----
In35_Human 179 VMLGFARDGVAQRLLCOICQVHSAFCWASSPSZSHSVCEMCDPEQ-----
CS1 104 .....GRSGATARECHAGVCYGWEGSASVPRPVHNGEHWGSKEL*ESLRM*XXRSEC*X-----

331fn 139 -----(SEQ ID NO:11)-----
In35_Human 239 PDILDGPELHDVLEIHFQKPTKGGCGRCPDSRTPTAGPSSLHL-----
CS1 156 *VASNSSLIYWCSXS*ALGLAPXMXSGRPNXISPIIXXOKXIPXSIXISIA (SEQ ID NO:12)
                                           (SEQ ID NO:13)
```

Figure 7



Abp2 1 RLRNGHVGISFVPKETGEHLVHVKKNGQHVASSIPVVISQSEIGDASRVVSGQGLHEG
C50 1 -----
C57 1 -----

Abp2 61 HTFEPAEFIIDTRDAGYGGLSLSIEGFSKVDINTEDLEDGTCRVTYCPTTEPGNYIINIKF
C50 1 -----
C57 1 -----HEGRPTTEPGNYIINIKF

Abp2 121 ADQHVPGPSFFSVKVTGEGRVKESITRRRRAPSVANVGSHCDLSLKIPEISIQDMTAQVTS
C50 1 -----
C57 18 ADQHVPGPSFFSVKVTGEGRVKESITRRRRAPSVANVGSHCDLSLKIPEISIQDMTAQVTS

Abp2 181 PSGKTHEAEIVEGENHTYCIREFVPAEMGTHTVSVKYKGQHVPGSPFFQFTVGPLGEGGAHK
C50 1 -----
C57 78 PSGKTHEAEIVEGENHTYCIREFVPAEMGTHTVSVKYKGQHVPGSPFFQFTVGPLGEGGAHX

Abp2 241 VRAGGPGLLENEGVPPEFS.TWTREAGAGGLAVEDEKAEISFEDRQDESCGWAYVV
C50 1 -----
C57 138 VRAGGPGLLENEGVPPEFS.TWTREAGAGGLAVEDEKAEISFEDRQDESCGWAYVV

Abp2 300 QEPGDYEVSVKFNEEHIPDSFFVVPVASPSGDARRLTVSSSLQESGLKVNQPASFVSLNG
C50 1 -----
C57 197 XEPDS* XNPXQVSTKEHX-----

Abp2 360 AKGAIDAKVHSPSGALEECYVTEIDQDKYAVRFIPRENGVYLIDVKFNGTHIPGSPFKIR
C50 1 -----
C57 214 -----

Abp2 420 VGEFGHGGDPGLVSAYGAGLEG.GVTGNPAEFVVNTSNAGAGALSVTIDGPSKVKMDCQE
C50 1 -----HEGRGVTGNPAEFVVNTSNAGAGALSVTIDGPSKVKMDCQE
C57 214 -----

Abp2 479 CPEGYRVTYTPMAPGSYLSIKYGGPYHIGGSPFKAKVTGPRLVSNHSLHETSSVFVDSL
C50 42 CPEGYRVTYTPMAPGSYLSIKYGGPYHIGGSPFKAKVTGPRLVSNHSLHETSSVFVDSL
C57 214 -----

Abp2 539 TKATCAPQHGAFGPGPADASKVVAKGLGLSKAYVCKKSSFTVDCSKAGNMMLLVGVHGPW
C50 102 TKATCAPQHGAFGPGPADASKVVAKGLGLSKAYVCKKSSFTVDCSKAGNMMLLVGVHGPW
C57 214 -----

Abp2 599 TPCHEILVKRVGS.RLYSVSYLLKDKGE.YTLVVKWCHHEHFGSPYRVVVP (SEQ ID NO:14)
C50 162 TPCHEILVKRVGS.RLYSVSYLLKDKGE.YTLVVKWCHHEHFGSPYRVVVP (SEQ ID NO:15)
C57 214 TPCHEILVKRVGS.RLYSVSYLLKDKGE.YTLVVKWCHHEHFGSPYRVVVP (SEQ ID NO:16)

Figure 8